



A-688A.ST25.txt  
SEQUENCE LISTING

<110> FEIGE, ULRICH  
KOHNO, TADAHIKO  
LACEY, DAVID LEE  
BOONE, THOMAS CHARLES

<120> INTEGRIN/ADHESION ANTAGONISTS

<130> A-688A

<140> 09/840,277  
<141> 2001-04-23

<150> 60/198,919  
<151> 2000-04-21

<150> 60/201,394  
<151> 2000-05-03

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<170> PatentIn version 3.1

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ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc 96  
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
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atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc 144  
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
35 40 45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag 192  
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
50 55 60

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Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
65 70 75 80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat 288  
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
85 90 95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc 336  
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
100 105 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag 384  
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
115 120 125

## A-688A.ST25.txt

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agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc g <sup>t</sup> g Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val 145 150 155 160	480
gag tgg gag agc aat ggg cag cc <sup>g</sup> gag aac aac tac aag acc acg cct Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro 165 170 175	528
ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr 180 185 190	576
gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc g <sup>t</sup> g Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val 195 200 205	624
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Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser 35 40 45	
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu 50 55 60	
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr 65 70 75 80	
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn 85 90 95	
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro 100 105 110	
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Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
165 170 175

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
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Ser Gln

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<212> PRT  
<213> Artificial Sequence

<220>  
<223> Selectin antagonist peptide

<400> 76

His Arg Ala Glu Trp Leu Ala Leu Trp Glu Gln Met Ser Pro  
1 5 10

<210> 77  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
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<400> 77

Lys Lys Glu Asp Trp Leu Ala Leu Trp Arg Ile Met Ser Val  
1 5 10

<210> 78  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
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<400> 78

Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys  
1 5 10

<210> 79  
<211> 12  
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<220>  
<223> Selectin antagonist peptide

<400> 79

Asp Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys  
1 5 10

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<210> 80  
<211> 12  
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<220>  
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<400> 80

Asp Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys  
1 5 10

<210> 81  
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<212> PRT  
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<220>  
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<400> 81

Asp Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys  
1 5 10

<210> 82  
<211> 16  
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<220>  
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<400> 82

Cys Gln Asn Arg Tyr Thr Asp Leu Val Ala Ile Gln Asn Lys Asn Glu  
1 5 10 15

<210> 83  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
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<400> 83

Ala Glu Asn Trp Ala Asp Asn Glu Pro Asn Asn Lys Arg Asn Asn Glu  
1 5 10 15

Asp

<210> 84  
<211> 19  
<212> PRT  
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<220>  
<223> Selectin antagonist peptide

<400> 84

Arg Lys Asn Asn Lys Thr Trp Thr Trp Val Gly Thr Lys Lys Ala Leu  
1 5 10 15

Thr Asn Glu

<210> 85

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Selectin antagonist peptide

<400> 85

Lys Lys Ala Leu Thr Asn Glu Ala Glu Asn Trp Ala Asp  
1 5 10

<210> 86

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Selectin antagonist peptide

<220>

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<222> (3 and)..(15)

<223> Xaa is any amino acid residue

<400> 86

Cys Gln Xaa Arg Tyr Thr Asp Leu Val Ala Ile Gln Asn Lys Xaa Glu  
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<210> 87

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Selectin antagonist peptide

<220>

<221> misc\_feature

<222> (13 and)..(15)

<223> Xaa is any amino acid residue

<400> 87

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Asp

<210> 88  
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<220>  
<223> Vinculin binding peptide

<400> 88

Ser Ser Gln Asn Trp Asp Met Glu Ala Gly Val Glu Asp Leu Thr Ala  
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Ala Met Leu Gly Leu Leu Ser Thr Ile His Ser Ser Ser Arg  
20 25 30

<210> 89  
<211> 31  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Vinculin binding peptide

<400> 89

Ser Ser Pro Ser Leu Tyr Thr Gln Phe Leu Val Asn Tyr Glu Ser Ala  
1 5 10 15

Ala Thr Arg Ile Gln Asp Leu Leu Ile Ala Ser Arg Pro Ser Arg  
20 25 30

<210> 90  
<211> 31  
<212> PRT  
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<220>  
<223> Vinculin binding peptide

<400> 90

Ser Ser Thr Gly Trp Val Asp Leu Leu Gly Ala Leu Gln Arg Ala Ala  
1 5 10 15

Asp Ala Thr Arg Thr Ser Ile Pro Pro Ser Leu Gln Asn Ser Arg  
20 25 30

<210> 91  
<211> 18  
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<220>  
<223> Vinculin binding peptide

<400> 91

Asp Val Tyr Thr Lys Lys Glu Leu Ile Glu Cys Ala Arg Arg Val Ser  
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Glu Lys

<210> 92  
<211> 27  
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<220>  
<223> Vinculin binding peptide

<400> 92

Ser Thr Gly Gly Phe Asp Asp Val Tyr Asp Trp Ala Arg Gly Val Ser  
1 5 10 15

Ser Ala Leu Thr Thr Thr Leu Val Ala Thr Arg  
20 25

<210> 93  
<211> 27  
<212> PRT  
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<220>  
<223> Vinculin binding peptide

<400> 93

Ser Thr Gly Gly Phe Asp Asp Val Tyr Asp Trp Ala Arg Arg Val Ser  
1 5 10 15

Ser Ala Leu Thr Thr Thr Leu Val Ala Thr Arg  
20 25

<210> 94  
<211> 30  
<212> PRT  
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<220>  
<223> Vinculin binding peptide

<400> 94

Ser Arg Gly Val Asn Phe Ser Glu Trp Leu Tyr Asp Met Ser Ala Ala  
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Met Lys Glu Ala Ser Asn Val Phe Pro Ser Arg Arg Ser Arg  
20 25 30

<210> 95  
<211> 19  
<212> PRT  
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<220>  
<223> Laminin related peptide |

<400> 95

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Arg Glu Asp Val Glu Ile Leu Asp Val Tyr Ile Gly Ser Arg Pro Asp  
1 5 10 15

Ser Gly Arg

<210> 96  
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<220>  
<223> Laminin related peptide

<400> 96

Tyr Ile Gly Ser Arg Arg Glu Asp Val Glu Ile Leu Asp Val Pro Asp  
1 5 10 15

Ser Gly Arg

<210> 97  
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ggggggcata tggaatgtga atctggtcca tgctgcagaa actg

44

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<400> 98

taagttcttg aaggaaggta ccatctgtaa gagagctaga ggtg

44

<210> 99  
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<212> DNA  
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<220>  
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<400> 99

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44

<210> 100  
<211> 51  
<212> DNA  
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A-688A.ST25.txt

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<223> Used to form echistatin template for PCR

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cgtccatgtc gtcacacctta gctc 24

<210> 103  
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<212> DNA  
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<223> Used to form echistatin template for PCR

<400> 103  
gtgtgggtt ctcggggcagt caca 24

<210> 104  
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<210> 105  
<211> 48  
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<400> 105  
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<210> 106

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<211> 22  
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 aacataagta cctgttaggat cg 22

<210> 107  
 <211> 49  
 <212> DNA  
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 <223> PCR primer  
  
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<210> 108  
 <211> 859  
 <212> DNA  
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 <223> NdeI site

<220>  
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 <222> (854)..(854)  
 <223> BamHI site

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 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
 1 5 10 15

ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc 96  
 Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
 20 25 30

ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg 144  
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val  
 35 40 45

agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg 192  
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
 50 55 60

gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc 240  
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

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65

70

75

acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg	288
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu	
80 85 90 95	
aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc	336
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala	
100 105 110	
ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca	384
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro	
115 120 125	
cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag	432
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln	
130 135 140	
gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc	480
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala	
145 150 155	
gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg	528
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr	
160 165 170 175	
cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc	576
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu	
180 185 190	
acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc	624
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser	
195 200 205	
gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc	672
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser	
210 215 220	
ctg tct ccg ggt aaa ggt gga ggt ggt ggt gaa tgt gaa tct ggt cca	720
Leu Ser Pro Gly Lys Gly Gly Gly Gly Glu Cys Glu Ser Gly Pro	
225 230 235	
tgc tgc aga aac tgt aag ttc ttg aag gaa ggt acc atc tgt aag aga	768
Cys Cys Arg Asn Cys Lys Phe Leu Lys Glu Gly Thr Ile Cys Lys Arg	
240 245 250 255	
gct aga ggt gac gac atg gac gac tac tgt aac ggt aag acc tgt gac	816
Ala Arg Gly Asp Asp Met Asp Asp Tyr Cys Asn Gly Lys Thr Cys Asp	
260 265 270	
tgc ccg aga aac cca cac aag ggt cca gct act taatggatcc	859
Cys Pro Arg Asn Pro His Lys Gly Pro Ala Thr	
275 280	

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<220>  
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<220>  
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<223> NdeI site

<220>  
<221> misc\_feature  
<222> (854)..(854)  
<223> BamHI site

<400> 109

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1 5 10 15

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser  
35 40 45

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
65 70 75 80

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
85 90 95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
100 105 110

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
115 120 125

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
165 170 175

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
210 215 220

Ser Pro Gly Lys Gly Gly Gly Gly Glu Cys Glu Ser Gly Pro Cys  
225 230 235 240

Cys Arg Asn Cys Lys Phe Leu Lys Glu Gly Thr Ile Cys Lys Arg Ala

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245

250

255

Arg Gly Asp Asp Met Asp Asp Tyr Cys Asn Gly Lys Thr Cys Asp Cys  
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Pro Arg Asn Pro His Lys Gly Pro Ala Thr  
275 280

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<223> AatII_site
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<222> (140)..(140)
<223> clai site
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catacagata accatctgcg gtgataaaatt atctctggcg gtgttgacat aaataccact 120
ggcggtgata ctgagcacat 140
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<210> 111
<211> 55
<212> DNA
<213> Artificial Sequence
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<220>  
<223> pAMG21

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<221> misc_feature
<222> (1)..(1)
<223> ClaI site
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<220>
<221> misc_feature
<222> (55)..(55)
<223> KpnI site
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<400> 111  
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<210> 112
<211> 1546
<212> DNA
<213> Artificial Sequence
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<220>  
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<223> AatII sticky end

<220>  
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<223> SacII sticky end

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ctcctgagta	ggacaaatcc	gccgggagcg	gatttgaacg	ttgcgaagca	acggcccgga	180
gggtggcggg	caggacgccc	gccataaact	gccaggcatc	aaattaagca	gaaggccatc	240
ctgacggatg	gccttttgc	gtttctacaa	actctttgt	ttattttct	aaatacattc	300
aaatatggac	gtcgactta	actttaaag	tatggcaat	caattgctcc	tgttaaaatt	360
gcttagaaa	tacttggca	gcgggttgtt	gtattgagtt	tcatttgcgc	attggtaaa	420
tggaaagtga	ccgtgcgcct	actacagcct	aatattttg	aaatatccca	agagctttt	480
cttcgcatg	cccacgctaa	acattcttt	tctttttgg	ttaaatcggt	gtttgattta	540
ttatttgcta	tatattttt	tcgataatta	tcaactagag	aaggaacaat	taatggatg	600
ttcatacacg	catgtaaaaaa	taaactatct	atatagttgt	ctttctctga	atgtgaaaaa	660
ctaagcattc	cgaagccatt	attagcagta	tgaatagggaa	aactaaaccc	agtgataaga	720
cctgatgatt	tcgcttcttt	aattacattt	ggagattttt	tatttacagc	attgtttca	780
aatatattcc	aattaatcg	tgaatgattt	gagttagaat	aatctactat	aggatcatat	840
tttatttaat	tagcgtcatc	ataatattgc	ctccattttt	taggtaatt	atccagaatt	900
gaaatatcag	attnaaccat	agaatgagga	taaatgatcg	cgagtaata	atattcacaa	960
tgtaccattt	tagtcatatc	agataagcat	tgattaatat	cattattgct	tctacaggct	1020
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ttatccttac	ctattgtttg	tcgcaagttt	tgcgtgttat	atatcattaa	aacggtaata	1140
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aattgtttaa	cataagtacc	tgttaggatcg	tacaggttta	cgcaagaaaa	tggttgtta	1260
tagtcgatta	atcgatttga	ttctagattt	gttttaacta	attaaaggag	gaataacata	1320
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actcgaggat	ccgcggaaag	aagaagaaga	agaagaaagc	ccgaaaggaa	gctgagttgg	1440
ctgctgccac	cgctgagcaa	taactagcat	aacccttgg	ggcctctaaa	cgggtcttga	1500
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gataatatat gagcacaaaaa aagaaaaccat taacacaaga gcagctttag gacgcacgac 180  
gccttaaagc aatttatgaa aaaaagaaaaa atgaacttgg cttatcccag gaatctgtcg 240  
cagacaagat ggggatgggg cagtcaggcg ttggtgcttt attaatggc atcaatgcat 300  
taaatgctta taacgcccga ttgcttacaa aaattctcaa agtttagcggtt gaagaattta 360  
gcccttcaat cgccagagaa tctacgagat gtatgaagcg gtttagtatgc agccgtcact 420  
tagaagttagtac ctgtttttc tcatgttcag gcagggatgt tctcacctaa 480  
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tagcggtcag gtgttttac aaccactaaa cccacagtac ccaatgatcc catgcaatga 780  
gagttgttcc gttgtgggaa aagttatcgc tagtcagtgg cctgaagaga cgtttggctg 840  
atagactagt ggatccacta gtgtttctgc cc 872

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agtatgccgg tgtctttat cagaccgttt cccgcgttgtt gaaccaggcc agccacgttt 180  
ctgcgaaaac gcgggaaaaaa gtcgaagcgg cgatggcgg gctgaattac attcccaacc 240  
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gtgccagcgt ggtgggtgtcg atggtagaac gaagcggcgt cgaaggctgt aaagcggcgg 420  
tgcacaatct tctcgccaa cgcgtcagtg ggctgatcat taactatccg ctggatgacc 480  
aggatgccat tgctgtggaa gctgcctgca ctaatgttcc ggcgttattt cttgatgtct 540

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ctgaccagac acccatcaac agtattattt	tctccatga agacggtacg	cgactggcg	600
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ctgtctcgcc	gcgtctgcgt ctggctggct	ggcataaata	720
agccgatagc	ggaacggaa ggcgactgga	gtgccatgtc	780
aatgctgaa	tgagggcatc	gttcccactg	840
tgggcgcaat	gcgcgccatt	accgagtccg	900
tgggatacga	cgataccgaa	gacagctcat	960
aggatttcg	cctgctgggg	caaaccagcg	1020
aggcggtgaa	gggcaatcag	ctgtgccccg	1080
cgcacaatac	gcaaaccgcc	tctcccccg	1140
gacaggttcc	ccgactggaa	agcggacagt	1197
	aaggtaccat	aggatccagg	
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<210> 115

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Laminin related peptide

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<210> 116

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Laminin related peptide

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<210> 117

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> Laminin related peptide

<400> 117

Met Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg  
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Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg  
20 25

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<210> 118  
<211> 26  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Laminin related peptide

<400> 118

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1 5 10 15

Trp Met Leu Ala Arg Gly Gly Gly Gly  
20 25

<210> 119  
<211> 25  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Laminin related peptide

<400> 119

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1 5 10 15

Asp Ser Gly Arg Gly Gly Gly Gly  
20 25

<210> 120  
<211> 20  
<212> PRT  
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<220>  
<223> Laminin related peptide

<400> 120

Met Arg Gly Asp Arg Gly Asp Tyr Ile Gly Ser Arg Arg Gly Asp Gly  
1 5 10 15

Gly Gly Gly Gly  
20

<210> 121  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Encoding Laminin related peptide, for PCR reaction to yield in-frame fusion to Fc

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A-688A.ST25.txt

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<220>  
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Ile Gly Ser Arg Tyr Ile Gly Ser Arg  
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Met Leu Ala Arg  
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Ser Gly Arg

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A-688A.ST25.txt

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Ile Gly Ser Arg Tyr Ile Gly Ser Arg  
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